

SEQUENCE LISTING

<110> Ledbetter, Jeffrey

Hayden-Ledbetter, Martha

<120> Binding Domain-Immunoglobulin Fusion Proteins

<130> 390069.401

<140> US

<141> 2002-01-17

<150> US 09/765,208

<151> 2001-01-17

<160> 38

<170> PatentIn version 3.0

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<223> SYNTHETIC MOUSE-HUMAN CHIMERIC FUSION GENE

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<222> (13)..(807)<223> MOUSE ANTI-HUMAN CD20 SCFV

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<221> C_region
<222> (808)..(1513)<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES
PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUN
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<222> (13)..(807)

<223> MOUSE ANTI-HUMAN CD20 SCFV

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<223> HINGE CYSTEINES MUTATED TO SERINES (826-829; 844-847; 853-856)
WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS

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 <223> HINGE CYSTEINES MUTATED TO SERINES (19-21; 37-39; 46-48)

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<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

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<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

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<400> 10		
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aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact	120	
atgaactgta agtccagtc aagtgttttc tacagttcaa atcagaggaa ttatggcc	180	
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg	240	
gaatctggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc	300	
atcagcagtg tacatactga agacctggca gtttattact gtcataatt cctctttcg	360	
tggacgttcg gtggaggcac caagctggaa atcaaaggcg gtggtggttc gggtggtggt	420	
ggttcgggtg gcggcggatc ttctcaggc caactgcagc agcctgggc tgaactggtg	480	
aagcctggga cttcagtgaa gctgtcctgc aaggcctctg gctacacctt caccaactac	540	
tggatggtct gggtaagca gacgcctgga gaaggccttg agtggattgg agaaattatt	600	
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca	660	
gacaaatcct cccgcacagc ctacatgcaa ctcagcagcc tggcatctga ggactctgcg	720	
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggttgctt	780	
actggggcca agggactctg gtcactgtct ctgcagcctg atca	824	

<210> 11

<211> 266

<212> PRT

<213> Mus musculus

<220>
<221> INIT_MET
<222> (1)..(1)

<220>
<221> SIGNAL
<222> (1)..(22)

<220>
<221> DOMAIN
<222> (23)..(128)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<220>
<221> SITE
<222> (129)..(144)
<223> ASP-(GLY3SER)-(GLY4SER) 2-SER LINKER PEPTIDE

<220>
<221> DOMAIN
<222> (145)..(266)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

```

<400> 11

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1           5           10           15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20          25          30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35          40          45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser

```

50

55

60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp
 260 265

<210> 12

<211> 271

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)...(271)

<223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10				15		
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala
					20		25						30		
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser
					35		40				45				
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro
					50		55			60					
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser
					65		70			75			80		
Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
					85			90			95				
Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys
					100			105				110			
Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Thr	Lys	Leu	
					115			120			125				
Glu	Ile	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly		
					130		135			140					
Gly	Ser	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg
					145		150			155			160		
Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe
					165			170			175				
Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
					180			185			190				
Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn
					195			200			205				
Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	Ser
					210		215			220					
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val
					225		230			235			240		
Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	Tyr	
					245			250			255				
Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	
					260			265			270				

<210> 13
 <211> 259
 <212> PRT
 <213> Mus musculus

<220>

<221> SITE
 <222> (1)..(259)
 <223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr
 1 5 10 15

Gly Gly Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
 20 25 30

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
 35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
 50 55 60

Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser
 100 105 110

Asp Asn Pro Trp Thr Phe Gly Gly Thr Glu Leu Glu Ile Lys Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ala
 130 135 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser
 145 150 155 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
 165 170 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
 180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
 195 200 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
 210 215 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 245 250 255

Val Ser Ser

<210> 14

<211> 272

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(272)

<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser
 35 40 45

Val Phe Tyr Ser Ser Asn Gln Arg Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Val His Thr Glu Asp Leu Ala Val Tyr
 100 105 110

Tyr Cys His Gln Phe Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys
 115 120 125

Leu Glu Ile Lys Gly Gly Ser Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val
 145 150 155 160

Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 165 170 175

Phe Thr Asn Tyr Trp Met Val Trp Val Lys Gln Thr Pro Gly Glu Gly
 180 185 190

Leu Glu Trp Ile Gly Glu Ile Ile Pro Ser Asn Gly Arg Thr Lys Tyr
 195 200 205

Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220

Arg Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala
 225 230 235 240

Val Tyr Tyr Cys Ala Arg Glu Met Ser Ile Ile Thr Thr Val Leu Thr
 245 250 255

Pro Gly Leu Leu Thr Gly Ala Lys Gly Leu Trp Ser Leu Ser Leu Gln
 260 265 270

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)
 <223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys

260

265

270

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 16

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>

<221> DOMAIN

<222> (265)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
130 135 140Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 17

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
 260 265 270

Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
 275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE
 <222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN
 <222> (266)..(288)

<223> WILD TYPE IGA HINGE

<220>

<221> DOMAIN
<222> (289)..(505)

<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
				20				25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
				35			40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
				50			55				60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	65				70				75				80		
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85			90					95			
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105					110			
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
	115					120					125				
Asp	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser		
	130				135			140							
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
	145				150				155				160		
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165				170					175			
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
	180					185						190			
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
	195					200						205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210				215					220					
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys

225	230	235	240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr		Trp Tyr Phe Asp Val Trp	
245		250	255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr			
260	265		270
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys			
275	280		285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys			
290	295		300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
305	310	315	320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr			
325	330		335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu			
340	345		350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			
355	360		365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys			
370	375		380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln			
385	390	395	400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu			
405		410	415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro			
420	425		430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn			
435	440		445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu			
450	455		460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
465	470	475	480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln			
485		490	495
Lys Ser Leu Ser Leu Ser Pro Gly Lys			
500		505	

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)
WILD TYPE CH2 AND CH3 DOMAINS
ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1 5 10 15

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
20 25 30

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
35 40 45

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
50 55 60

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
65 70 75 80

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
85 90 95

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
100 105 110

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
115 120 125

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
130 135 140

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
145 150 155 160

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
165 170 175

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
180 185 190

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE
 <222> (1)..(23)

<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>

<221> DOMAIN
 <222> (24)..(240)
 <223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
 20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 100 105 110

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 115 120 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 130 135 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 145 150 155 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 165 170 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 180 185 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 195 200 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 210 215 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230 235 240

<210> 21

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (1)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1455)

<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
 aagcttgcgg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcctca 60
 gtcataatttgcagaggaca aattgttctc tcccagtctc cagcaatcct gtctgcattct
 ccagggaga aggtcacaat gacttgcagg gccagctcaa gtgttaactt catgcactgg
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct
 tctggagtcc ctgctcgctt cagttggcagt gggctggga cctcttactc tctcacaatc
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
 cccacgttcg gtgctggac caagctggag ctgaaagatg gcgggtggctc gggcggtgg
 gatatctggag gaggtgggag ctctcaggct tatctacagc agtctgggc tgagctgg
 aggccctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttt
 ccagggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
 gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctg
 gtcttatttct gtgcaagagt ggtgtactat agtaactctt actggactt cgatgtctgg
 ggcacaggaa ccacggcac cgtctctgat ccaagaaggt tggacaagat agaagatgaa
 aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa
 agatccttat ctttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttgtgaag
 gatataatgt taaacaaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaaggt
 gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct
 gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aaccctggaa
 aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc
 ttctgttcca atcgggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag
 tccccggta gattcgagag aatcttactc agagctgcaa atacccacag ttccgccaaa
 ctttgcggc aacaatccat tcacttggga ggagtatttgcatttgc aatttgcacc
 gtgtttgtca atgtgactga tccaaagccaa gtgagccatg gcactggctt cacgtccctt
 ggcttactca aactcgagtg ataatctaga 1470

<210> 22

<211> 1290
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MOUSE-HUMAN HYBRID

<220>
 <221> misc_feature
 <222> (13)..(808)
 <223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
 <221> misc_feature
 <222> (814)..(1275)
 <223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaat cagtgcttca 60
 gtcataattt ccagaggaca aatttgttctc tcccagtcctc cagcaatcct gtctgcattt
 ccagggaga aggtcacaat gacttgcagg gccagctcaa gtgttaaggta catgcactgg 120
 taccaggaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct
 tctggagtcc ctgctcgctt cagtgccagt gggctctggga cctcttactc tctcacaatc 180
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 240
 cccacgttcg gtgctggac caagctggag ctgaaagatg gcggggctc gggcggtgg 300
 gatatctggag gaggtggag ctctcaggct tatctacagc agtctggggc tgagctggtg 360
 aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 420
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 480
 ccagggaaatg gtgataacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 540
 gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgctg 600
 gtctatattct gtgcaagagt ggtgtactat agtaactctt actggacttt cgatgtctgg 660
 720
 780

Sequence Data for the Human Genome

ggcacaggga ccacggtcac cgtctctgat ccagaaaaca gcttgaaat gaaaaaggt 840
 gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct 900
 gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aaccctggaa 960
 aatggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtccacc 1020
 ttctgttcca atcgggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag 1080
 tccccggta gattcgagag aatcttactc agagctgcaa atacccacag ttccgccaaa 1140
 ccttgcgggc aacaatccat tcacttggga ggagtattt aattgcaacc aggtgcttcg 1200
 gtgttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccctt 1260
 ggcttactca aactcgagtg ataatctaga 1290

<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23
 gtcaagcttg ccgccatgga ttttcaagtg cagattttc agc 43

<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 24
 gtcgtcgagc tcccacctcc tccagatcca ccaccgcccc agccaccggcc acctttcagc 60

tccagcttgg tccc

74

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 25

gctgctgagc tctcaggctt atctacagca agtctgg

37

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 26

gttgtctgat cagagacggt gaccgtggtc cc

32

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 27

gttgtcggat ccagaaaaca gctttgaaat gcaa 34

<210> 28

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 28 gttgtttcta gattatcact cgagtttgag taagccaaag gacg 44

<210> 29

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 29 gttgtcggat ccaagaaggt tggacaagat agaag 35

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 30

and the *Leucanthemum* and *Thlaspi* are the only species which have been found to contain any appreciable amount of saponin.

gtcttatataa gcagagctct ggc 23

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 31 25

cgaggctgat cagcgagctc tagca

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 32 25

ccgcaatttg aggattctga tcacc

<210> 33

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN
 <222> (268)..(481)
 <223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125

Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
 130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe

195

200

205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255

Gly Thr Gly Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
 260 265 270

Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
 275 280 285

Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
 290 295 300

Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
 305 310 315 320

Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
 325 330 335

Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
 340 345 350

Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
 355 360 365

Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
 370 375 380

Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
 385 390 395 400

Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
 405 410 415

Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
 420 425 430

Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
 435 440 445

Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460

Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480

Leu Glu

<210> 34
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
 <221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN SCFV

<220>
 <221>
 DOMAIN
 <222> (268)..(421)
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10				15		

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
							20		25				30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
							35		40			45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
					50		55				60				

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
				65		70			75				80		

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
					85			90			95				

Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
							100		105			110			

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 305 310 315 320
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 325 330 335
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 340 345 350
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 355 360 365
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 370 375 380
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 385 390 395 400
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 405 410 415

Gly Leu Leu Lys Leu Glu
420

<210> 35

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> N_region
<222> (1)..(63)

<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35

ccagttccct caactccacc taccccatct ccctcaactc cacctacccc atctccctca 60

tgc

63

<210> 36

<211> 21

<212> PRT

<213> Homo sapiens

<400> 36

Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr
1				5				10				15			

Pro	Ser	Pro	Ser	Cys
			20	

<210> 37

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(6)

<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>

<221> N_region
<222> (8)..(752)<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37		
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc	60	
tccctcatgc tgccacccccc gactgtcact gcaccgaccg gccctcgagg acctgcttt	120	
aggttcagaa gcgatcctca cgtgcacact gaccggcctg agagatgcct caggtgtcac	180	
cttcacctgg acgcccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct	240	
ctgtggctgc tacagcgtgt ccagtgtctt gccgggctgt gccgagccat ggaaccatgg	300	
gaagaccttc acttgcactg ctgcctaccc cgagtccaaag acccccctaa ccgcccaccc	360	
ctcaaaatcc ggaaacacat tccggccga ggtccacctg ctggccgcgc cgtcggagga	420	
gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gccccaaagga	480	
tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg	540	
ggcatcccg caggagccca gccagggcac caccaccc cgtgtgacca gcatactgcg	600	
cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattggc gccacgaggc	660	
cctggccctg gcattcacac agaagaccat cgaccgcttgcgggtaaac ccacccatgt	720	
caatgtgtct gttgtcatgg cgagggtgga ctgataatct aga	763	

<210> 38

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (3)..(250)

<223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE ATTACHMENT TO SECRETORY COMPOUN

<400> 38

Asp	Gln	Pro	Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro
1				5				10						15	
Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg
						20		25						30	
Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys
						35		40						45	
Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr
					50			55				60			
Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Pro	Asp	Arg	Asp	Leu
					65		70		75				80		
Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro
					85			90					95		
Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser
					100		105					110			
Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg
					115		120					125			
Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn
					130		135				140				
Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp
					145		150		155				160		
Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys
					165			170					175		
Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr
					180		185				190				
Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys
					195		200				205				
Gly	Asp	Thr	Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala
					210		215				220				
Phe	Thr	Gln	Lys	Thr	Ile	Asp	Arg	Leu	Ala	Gly	Lys	Pro	Thr	His	Val
					225		230				235			240	

Asn Val Ser Val Val Met Ala Glu Val Asp
245 250